

RESULT 1

BCDO_CHICK

ID BCDO_CHICK STANDARD; PRT; 526 AA.
AC Q9I993;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Beta,beta-carotene 15,15'-dioxygenase (EC 1.14.99.36) (Beta-carotene
dioxygenase 1).

GN BCDO.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=LSL Lohmann; TISSUE=Duodenum;

RX MEDLINE=20261261; PubMed=10799297;

RA Wyss A., Wirtz G.M., Woggon W.D., Brugger R., Wyss M., Friedlein A.,
RA Bachmann H., Hunziker W.;

RT "Cloning and expression of beta,beta-carotene-15,15'-dioxygenase.";
RL Biochem. Biophys. Res. Commun. 271:334-336(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=LSL Lohmann; TISSUE=Duodenum;

RX MEDLINE=21134366; PubMed=11237856;

RA Wyss A., Wirtz G.M., Woggon W.D., Brugger R., Wyss M., Friedlein A.,
RA Riss G., Bachmann H., Hunziker W.;

RT "Expression pattern and localization of beta,beta-carotene 15,15'-
dioxygenase in different tissues.";

RL Biochem. J. 354:521-529(2001).

CC -!- FUNCTION: Symmetrically cleaves beta-carotene into two molecules
of retinal. The reaction proceeds in three stages, epoxidation of
the 15,15'-double bond, hydration of the double bond leading to
ring opening, and oxidative cleavage of the diol formed.

CC -!- CATALYTIC ACTIVITY: Beta-carotene + O(2) = 2 retinal.

CC -!- COFACTOR: Iron.

CC -!- PATHWAY: Vitamin A biosynthesis.

CC -!- SIMILARITY: Belongs to the beta-carotene dioxygenase family.

CC -----
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DR EMBL; AJ271386; CAB90825.1; -.

DR InterPro; IPR004294; RPE65.

DR Pfam; PF03055; RPE65; 1.

KW Dioxygenase; Oxidoreductase; Iron.

SQ SEQUENCE 526 AA; 60384 MW; 82C6EAAF75FE345B CRC64;

Query Match 100.0%; Score 2825; DB 1; Length 526;

Best Local Similarity 100.0%; Pred. No. 1.4e-191;

Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 METIFNRNKEEHPEPIKAEVQGQLPTWLQGVLLRNGPGMHTIGDTKYNHWFDGLALLHSF 60
|||
Db 1 METIFNRNKEEHPEPIKAEVQGQLPTWLQGVLLRNGPGMHTIGDTKYNHWFDGLALLHSF 60

Qy 61 TFKNGEVYYRSKYLRSDTYNCNIEANRIVVSEFGTMAYPDPCKNIFAKAFSYLSHTIPEF 120
|||
Db 61 TFKNGEVYYRSKYLRSDTYNCNIEANRIVVSEFGTMAYPDPCKNIFAKAFSYLSHTIPEF 120

Qy 121 TDNCLINIMKTGDDYYATSETNFIRKIDPQTLETLDKV DYSKYVAVNLATSHPHYDSAGN 180
|||
Db 121 TDNCLINIMKTGDDYYATSETNFIRKIDPQTLETLDKV DYSKYVAVNLATSHPHYDSAGN 180

Qy 181 ILNMGTSIVDKGRTKYVLFKIPSSVPEKEKKSCFKHLEVVCSIPSRSLLQPSYYHSFGI 240
|||
Db 181 ILNMGTSIVDKGRTKYVLFKIPSSVPEKEKKSCFKHLEVVCSIPSRSLLQPSYYHSFGI 240

Qy 241 TENYIVFIEQPFKLDIVKLATAYIRGVNWASCLSFKEDKTWFHFVDRKTKEVSTKFYT 300
|||
Db 241 TENYIVFIEQPFKLDIVKLATAYIRGVNWASCLSFKEDKTWFHFVDRKTKEVSTKFYT 300

Qy 301 DALVLYHHINAYEEDGHVVFDIVAYRDNSLYDMFYLK KLDKDFEVNNKLT SIPTCKRFVV 360
|||
Db 301 DALVLYHHINAYEEDGHVVFDIVAYRDNSLYDMFYLK KLDKDFEVNNKLT SIPTCKRFVV 360

Qy 361 PLQYDKDAEVGSNLVKLPTSATAVKEKDGSIYCQPEILCEGIELPRVNYDNGKKYKYVY 420
|||
Db 361 PLQYDKDAEVGSNLVKLPTSATAVKEKDGSIYCQPEILCEGIELPRVNYDNGKKYKYVY 420

Qy 421 ATEVQWSPVPTKIAKLNVQTKEVLHWGEDHCWPSEPIFVPSPDAREEDEGVVLTCVVSE 480
|||
Db 421 ATEVQWSPVPTKIAKLNVQTKEVLHWGEDHCWPSEPIFVPSPDAREEDEGVVLTCVVSE 480

Qy 481 PNKAPFLLILDRAFTKELGRATVNVEHMHD L HGMFIPQNDLGAETE 526
|||
Db 481 PNKAPFLLILDRAFTKELGRATVNVEHMHD L HGMFIPQNDLGAETE 526

RESULT 1

Q7ZTS0

ID Q7ZTS0 PRELIMINARY; PRT; 516 AA.
AC Q7ZTS0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Bcd01 protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Body;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Body;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC049331; AAH49331.1; -.
DR InterPro; IPR004294; RPE65.
DR Pfam; PF03055; RPE65; 1.
SQ SEQUENCE 516 AA; 58655 MW; DFBAC7D058736E53 CRC64;

Query Match 60.9%; Score 1720; DB 13; Length 516;
Best Local Similarity 59.9%; Pred. No. 3.7e-123;
Matches 311; Conservative 86; Mismatches 114; Indels 8; Gaps 5;

Qy 1 METIFNRNKEEHPEPIKAEVQGQLPTWLQGVLLRNGPGMHTIGDTKYNHWFDGLALLHSF 60
| : : :||||||| ||:| :| |:|| |:||||||| ::||| | |||||||:|||||||
Db 1 MQYDYGKNKEEHPEPIKTEVKGSIPPEWVQGTЛИRNGPGMFSVGETTYNHWFДGMALLHSF 60

Qy 61 TFKNGEVYYRSKYLRSDTYNCNIEANRIVVSEFGTMAYPDPCKNIFAKAFSYLSHTIPEF 120
||| |||:||| ||||| |::||| ||||| ||||||||| |||||:| :||| |||:

| | | | |
|----|-----|---|-----|
| Db | 61 | AINKGEVTYRSRYLRGDTYNNSMQANRIVVSEMGTMAYPDPCKNIFSKVITFLSHTIPDF | 120 |
| Qy | 121 | TDNCLINIMKTGDDYYATSETNFIRKIDPQTLETLDKVVDYSKYVAVNLATSHPHYDSAGN | 180 |
| | | | |
| Db | 121 | TDNCGNNIIKYGNDFHATSETNYIRKIDPVTLTQEKEIDYLKYLPVSIVASHTHYDKEGN | 180 |
| Qy | 181 | ILNMGTTSIVDKGRTKYVLFKIP-SSVPEKEKKSCFKLEVVCISPSRSLLQPSYYHSFG | 239 |
| : | : | : | : |
| Db | 181 | SYSMGTCIAEKGKTKYMLFKVPGESRPDGSP---LKSAAEVCTLPCRSLLTPSYYHSFG | 237 |
| Qy | 240 | ITENYIVFIEQPKLDIRKLATAYIRGVNWASCLSFKEDKTFHFVDRKTKEVSTKFY | 299 |
| : | : | : | : |
| Db | 238 | MTDNYFIFIEQPLKLDILKMATAYLRRVSWASCMFKHPEDSTLIHLIDRNTKKEVATKFY | 297 |
| Qy | 300 | TDALVLYHHINAYEEDGHVVFDIVAYRDNSLYDMFYLKLDKDFFEVNNKLTSIPTCKRFV | 359 |
| : | | : | |
| Db | 298 | TDAMTVYHQVNAFEDDGHVVFDVIAYDDNNLYEFFYLNKLKETMGATN-LYCKPKFTRFV | 356 |
| Qy | 360 | VPLQYDKDAEVGSNLVQLP-TSATAVKEKGSIYCQPEILCEGIELPRVNYYDNGKKYKY | 418 |
| | | | |
| Db | 357 | FPL--SDQGETGENLVKLKYTTASAVKEKGKIMCQGEVLCEGVELPRINYNFNGKKYRY | 414 |
| Qy | 419 | VYATEVQWSPVPTKIAKLNVQTKEVLHWGEDHCWPSEPIFVPSPDAREEDEGVVLTCAVV | 478 |
| | | : | : |
| Db | 415 | SYMCCVDESPVATRIVKFADTKQQIEWKGDDGFASEPVFIPRPGAVDEDGGVVLTIVI | 474 |
| Qy | 479 | SEPNKAPFLLILDAKTFKELGRATVNEMHLDLHGMFIP | 517 |
| :: | : | : | : |
| Db | 475 | NKPLQGGFLLVDAKSFKEIARACLDVEIHMDMHGYFIP | 513 |